



PCT09

410
7-12-02
P.C.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/869,079A

DATE: 05/23/2002

TIME: 16:17:51

Input Set : A:\JAB-1458.txt

Output Set: N:\CRF3\05232002\I869079A.raw

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5 <110> APPLICANT: Masure, Stefan
6 Richardson, Alan
11 <120> TITLE OF INVENTION: Human AKT-3
15 <130> FILE REFERENCE: 51869/001
C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/869,079A
C--> 21 <141> CURRENT FILING DATE: 2002-04-15
25 <150> PRIOR APPLICATION NUMBER: GB 9828375.7
27 <151> PRIOR FILING DATE: 1998-12-22
31 <160> NUMBER OF SEQ ID NOS: 3
35 <170> SOFTWARE: PatentIn Ver. 2.0
39 <210> SEQ ID NO: 1
41 <211> LENGTH: 1547
43 <212> TYPE: DNA
45 <213> ORGANISM: Homo sapiens
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59 ccagtggact actgttatag agagaacatt tcatgtagat actccagagg aaagggaaga 300
61 atggacagaa gctatccagg ctgtagcaga cagactgcag aggcaagaag aggagagaat 360
63 gaattgtagt ccaacttcac aaattgataa tataggagag gaagagatgg atgcctctac 420
65 aacccatcat aaaagaaaga caatgaatga ttttgactat ttgaaactac taggtaaagg 480
67 cacttttggg aaagtatttt tggttcgaga gaaggcaagt ggaaaatact atgctatgaa 540
69 gattctgaag aaagaagtca ttattgcaaa ggatgaagtg gcacacactc taactgaaag 600
71 cagagtatta aagaacacta gacatccctt tttaacatcc ttgaaatatt ccttcagac 660
73 aaaagaccgt ttgtgttttg tgatggaata tgttaatggg ggcgagctgt ttttccattt 720
75 gtcgagagag cgggtgttct ctgaggaccg cacacgtttc tatggtgcag aaattgtctc 780
77 tgccttggac tatctacatt ccggaaagat tgtgtaccgt gatctcaagt tggagaatct 840
79 aatgctggac aaagatggcc acataaaaaat tacagatttt ggactttgca aagaagggat 900
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83 gttagaagat aatgactatg gccgagcagt agactggtg ggcctagggg ttgtcatgta 1020
85 tgaaatgatg tgtgggaggt tacctttcta caaccaggac catgagaaac tttttgaatt 1080
87 aatattaatg tgtgggaggt aatttcctcg aacactctct tcagatgcaa aatcattgct 1140
89 ttcagggtct ttgataaagg atccaaataa acgccttggg ggaggaccag atgatgcaa 1200
91 agaaattatg agacacagtt tcttctctgg agtaaactgg caagatgtat atgataaaaa 1260
93 gcttgtacct ccttttaaac ctcaagtaac atctgagaca gatactagat attttgatga 1320
95 agaatttaca gctcagacta ttacaataac accacctgaa aaatatgatg aggatgggat 1380
97 ggactgcatg gacaatgaga ggcggccgca tttccctcaa ttttctact ctgcaagtgg 1440
99 acgagaataa gtctctttca ttctgtact tcaactgtcat cttcaattta ttactgaaaa 1500
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105 <210> SEQ ID NO: 2
107 <211> LENGTH: 1436

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109 <212> TYPE: DNA

111 <213> ORGANISM: Homo sapiens

115 <400> SEQUENCE: 2

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121 aaacctcaag atgtggattt accttatccc ctcaacaact ttccagtggc aaaatgccag 180
123 ttaatgaaaa cagaacgacc aaagccaaac acatttataa tcagatgtct ccagtggact 240
125 actgttatag agagaacatt tcatgtagat actccagagg aaagggaaga atggacagaa 300
127 gctatccagg ctgtagcaga cagactgcag aggcaagaag aggagagaat gaattgtagt 360
129 ccaacttcac aaattgataa tataggagag gaagagatgg atgcctctac aacctcatcat 420
131 aaaagaaaga caatgaatga ttttgactat ttgaaactac taggtaaagg cacttttggg 480
133 aaagtatttt tggttcgaga gaaggcaagt ggaaaatact atgctatgaa gattctgaag 540
135 aaagaagtca ttattgcaaa ggatgaagtg gcacacactc taactgaaag cagagtatta 600
137 aagaacacta gacatccctt tttaacatcc ttgaaatatt ccttcagac aaaagaccgt 660
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141 cgggtgttct ctgaggaccg cacacgtttc tatggtgcag aaattgtctc tgccttggac 780
143 tatctacatt ccggaagat tgtgtaccgt gatctcaagt tggagaatct aatgctggac 840
145 aaagatggcc acataaaaaa tacagatttt ggactttgca aagaagggat cacagatgca 900
147 gccaccatga agacattctg tggcactcca gaatatctgg caccagaggt gttagaagat 960
149 aatgactatg gccgagcagt agactggtgg ggcctagggg ttgtcatgta tgaaatgatg 1020
151 tgtgggaggt tacctttcta caaccaggac catgagaaac tttttgaatt aatattaatg 1080
153 gaagacatta aatttctctg aacactctct tcagatgcaa aatcattgct ttcagggtc 1140
155 ttgataaagg atccaaataa acgccttggg ggaggaccag atgatgcaaa agaaattatg 1200
157 agacacagtt tcttctctgg agtaaaactg caagatgtat atgataaaaa gcttgtacct 1260
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161 gctcagacta ttacaataac accacctgaa aaatatgatg aggatgggat ggactgcatg 1380
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173 <213> ORGANISM: Homo sapiens

177 <400> SEQUENCE: 3

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187 20 25 30
191 Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro
193 35 40 45
197 Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr
199 50 55 60
203 Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr
205 65 70 75 80
209 Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu
211 85 90 95
215 Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln
217 100 105 110
221 Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile
223 115 120 125
227 Gly Glu Glu Glu Met Asp Ala Ser Thr Thr His His Lys Arg Lys Thr

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235	145					150					155					160			
239	Lys	Val	Ile	Leu	Val	Arg	Glu	Lys	Ala	Ser	Gly	Lys	Tyr	Tyr	Ala	Met			
241					165					170						175			
245	Lys	Ile	Leu	Lys	Lys	Glu	Val	Ile	Ile	Ala	Lys	Asp	Glu	Val	Ala	His			
247				180					185					190					
251	Thr	Leu	Thr	Glu	Ser	Arg	Val	Leu	Lys	Asn	Thr	Arg	His	Pro	Phe	Leu			
253			195					200					205						
257	Thr	Ser	Leu	Lys	Tyr	Ser	Phe	Gln	Thr	Lys	Asp	Arg	Leu	Cys	Phe	Val			
259		210				215					220								
263	Met	Glu	Tyr	Val	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Ser	Arg	Glu			
265	225				230					235					240				
269	Arg	Val	Phe	Ser	Glu	Asp	Arg	Thr	Arg	Phe	Tyr	Gly	Ala	Glu	Ile	Val			
271				245					250					255					
275	Ser	Ala	Leu	Asp	Tyr	Leu	His	Ser	Gly	Lys	Ile	Val	Tyr	Arg	Asp	Leu			
277			260					265					270						
281	Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His	Ile	Lys	Ile	Thr			
283			275				280					285							
287	Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Thr	Asp	Ala	Ala	Thr	Met	Lys			
289		290				295					300								
293	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Glu	Asp			
295	305				310					315					320				
299	Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly	Val	Val	Met			
301				325				330						335					
305	Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	Asp	His	Glu			
307			340					345					350						
311	Lys	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Asp	Ile	Lys	Phe	Pro	Arg	Thr			
313			355				360					365							
317	Leu	Ser	Ser	Asp	Ala	Lys	Ser	Leu	Leu	Ser	Gly	Leu	Leu	Ile	Lys	Asp			
319		370				375					380								
323	Pro	Asn	Lys	Arg	Leu	Gly	Gly	Gly	Pro	Asp	Asp	Ala	Lys	Glu	Ile	Met			
325	385				390				395					400					
329	Arg	His	Ser	Phe	Phe	Ser	Gly	Val	Asn	Trp	Gln	Asp	Val	Tyr	Asp	Lys			
331				405				410					415						
335	Lys	Leu	Val	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser	Glu	Thr	Asp	Thr			
337			420					425					430						
341	Arg	Tyr	Phe	Asp	Glu	Glu	Phe	Thr	Ala	Gln	Thr	Ile	Thr	Ile	Thr	Pro			
343			435				440					445							
347	Pro	Glu	Lys	Tyr	Asp	Glu	Asp	Gly	Met	Asp	Cys	Met	Asp	Asn	Glu	Arg			
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VERIFICATION SUMMARY

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L:19 M:270 C: Current Application Number differs, Replaced Current Application Number

L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date